## Scientific and Technical Information Center
## SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA     Examiner # : 77512    Date: 6 – 15-05
Art Unit: 1635    Phone Number: 2-0765     Serial Number: 10/075,994
Location (Bldg/Room#): 2-D18 (Mailbox #): 2-C18   Results Format Preferred (circle): PAPER  DISK
*******************************************************************************

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Chemosensitizing w/ Liposomes

Inventors (please provide full names): U. Kasid et al.

CRFE

Earliest Priority Date: 2/15/02.

Search Topic:
*Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.*

*For Sequence Searches Only* *Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

please Search Seq ID No: 1 - 15 (NA)

$ - 50 NT Limit
- UNLimited size

please Search Interference &
Regular Data bas

Thanks.

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A nucleic - nucleic search, using sw model

Run on:     June 21, 2005, 05:25:39 ; Search time 3854 Seconds
                                         (without alignments)
                                         158.886 Million cell updates/sec

Title:            US-10-075-994A-1
Perfect score:    15
Sequence:         1 gtgctccattgatgc 15

Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched:         4554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters:     37698952

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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nucleic - nucleic search, using sw model

.on:        June 21, 2005, 05:32:48 ; Search time 6213 Seconds
                                     (without alignments)
                                     10.675 Million cell updates/sec

le:         US-10-075-994A-1
fect score: 15
uence:      1 gtgctccattgatgc 15

ring table: IDENTITY_NUC
            Gapop 10.0 , Gapext 1.0

rched:      13003524 seqs, 2210865434 residues

al number of hits satisfying chosen parameters:        22502830

imum DB seq length: 0
imum DB seq length: 50

t-processing: Minimum Match 0%
              Maximum Match 100%
              Listing first 45 summaries

abase :     Pending_Patents_NA_New:*
            1:  /cgn2_6/ptodata71/pna/PCT_NEW_COMB.seq:*
            2:  /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq2:*
            3:  /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
            4:  /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
            5:  /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
            6:  /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
            7:  /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
            8:  /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*
            9:  /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq3:*
            10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq4:*
            11: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq5:*
            12: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:*
            13: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq2:*
            14: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq3:*
            15: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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OM nucleic - nucleic search, using sw model

Run on:        June 21, 2005, 02:20:11 ; Search time 4129 Seconds
                                         (without alignments)
                                         148.304 Million cell updates/sec

Title:          US-10-075-994A-1
Perfect score:  15
Sequence:       1 gtgctccattgatgc 15

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters:        91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 02:27:36 ; Search time 907 Seconds
(without alignments)
73.058 Million cell updates/sec

Title: US-10-075-994A-1
Perfect score: 15
Sequence: 1 gtgctccattgatgc 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 12999316 seqs, 220877B887 residues

Total number of hits satisfying chosen parameters: 25598632

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq2:*
3: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
9: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq3:*
10: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq4:*
11: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq5:*
12: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:*
13: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq2:*
14: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq3:*
15: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model

Copyright GenCore version 5.1.6
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Run on:      June 21, 2005, 01:42:20 ; Search time 127 Seconds
                                       (without alignments)
                                       193.261 Million cell updates/sec

Title:           US-10-075-994A-1
Perfect score:   15
Sequence:        1 gtgctccattgatgc 15

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:      2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents NA:*
                 1:  /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2:  /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3:  /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4:  /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5:  /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6:  /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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OM nucleic - nucleic search, using sw model

Run on:         June 21, 2005, 05:16:12 ; Search time 126 Seconds
                                         (without alignments)
                                         194.795 Million cell updates/sec

Title:          US-10-075-994A-1
Perfect score:  15
Sequence:       1 gtgctccattgatgc 15

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:      1209694

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 listing first 45 summaries

Database :      Issued Patents_NA:*
                1:  /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                2:  /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                3:  /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                4:  /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                5:  /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*
                6:  /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                        SUMMARIES